

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/806,413A

DATE: 08/02/2001
TIME: 16:39:42

Input Set : A:\Q63731 Sequence Listing.txt
Output Set: N:\CRF3\08022001\I806413A.raw

ENTERED

3 <110> APPLICANT: Amano Enzyme, Inc.
5 <120> TITLE OF INVENTION: NOVEL ENZYME COMPOSITION AND PRODUCTION METHOD AND USE
THEREOF
7 <130> FILE REFERENCE: Q63731
9 <140> CURRENT APPLICATION NUMBER: 09/806,413A
C--> 10 <141> CURRENT FILING DATE: 2001-03-20
12 <150> PRIOR APPLICATION NUMBER: JP 10-294675
13 <151> PRIOR FILING DATE: 1998-09-30
15 <160> NUMBER OF SEQ ID NOS: 16
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 22
21 <212> TYPE: PRT
22 <213> ORGANISM: Aspergillus fumigatus
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27 1 5 10 15
30 Leu Ser Ser Ile Ala Ala
31 20
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35 <211> LENGTH: 22
36 <212> TYPE: PRT
37 <213> ORGANISM: Aspergillus fumigatus
39 <400> SEQUENCE: 2
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42 1 5 10 15
45 Gly Ala Ser Asp Leu Ser
46 20
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 28
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: synthetic DNA
57 <220> FEATURE:
58 <221> NAME/KEY: misc_feature
59 <222> LOCATION: (14)..(14)
60 <223> OTHER INFORMATION: "n" may be a c, g or t
63 <220> FEATURE:
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66 <223> OTHER INFORMATION: "n" may be a c, g or t
69 <220> FEATURE:
70 <221> NAME/KEY: misc_feature
71 <222> LOCATION: (20)..(20)
72 <223> OTHER INFORMATION: "n" may be a c, g or t
75 <400> SEQUENCE: 3
W--> 76 acgaattcaa ywsngcnggn aaytayaa OK

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79 <210> SEQ ID NO: 4
80 <211> LENGTH: 28
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: synthetic DNA
87 <220> FEATURE:
88 <221> NAME/KEY: misc_feature
89 <222> LOCATION: (17)..(17)
90 <223> OTHER INFORMATION: "n" may be a c, g or t
93 <220> FEATURE:
94 <221> NAME/KEY: misc_feature
95 <222> LOCATION: (23)..(23)
96 <223> OTHER INFORMATION: "n" may be a c, g or t
99 <220> FEATURE:
100 <221> NAME/KEY: misc_feature
101 <222> LOCATION: (26)..(26)
102 <223> OTHER INFORMATION: "n" may be a c, g or t
105 <400> SEQUENCE: 4
W--> 106 cggaattcta ytgysnaay wshgchgg OK 28
109 <210> SEQ ID NO: 5
110 <211> LENGTH: 28
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: synthetic DNA
117 <220> FEATURE:
118 <221> NAME/KEY: misc_feature
119 <222> LOCATION: (17)..(17)
120 <223> OTHER INFORMATION: "n" may be a c, g or t
123 <220> FEATURE:
124 <221> NAME/KEY: misc_feature
125 <222> LOCATION: (20)..(20)
126 <223> OTHER INFORMATION: "n" may be a c, g or t
129 <220> FEATURE:
130 <221> NAME/KEY: misc_feature
131 <222> LOCATION: (23)..(23)
132 <223> OTHER INFORMATION: "n" may be a c, g or t
135 <220> FEATURE:
136 <221> NAME/KEY: misc_feature
137 <222> LOCATION: (26)..(26)
138 <223> OTHER INFORMATION: "n" may be a c, g or t
141 <400> SEQUENCE: 5
W--> 142 tcaagcttgc raarttngch cchgchgg OK 28
145 <210> SEQ ID NO: 6
146 <211> LENGTH: 28
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:

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151 <223> OTHER INFORMATION: synthetic DNA
153 <220> FEATURE:
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156 <223> OTHER INFORMATION: "n" may be a c, g or t
159 <220> FEATURE:
160 <221> NAME/KEY: misc_feature
161 <222> LOCATION: (17)..(17)
162 <223> OTHER INFORMATION: "n" may be a c, g or t
165 <220> FEATURE:
166 <221> NAME/KEY: misc_feature
167 <222> LOCATION: (23)..(23)
168 <223> OTHER INFORMATION: "n" may be a c, g or t
171 <400> SEQUENCE: 6
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175 <210> SEQ ID NO: 7
176 <211> LENGTH: 1401
177 <212> TYPE: DNA
178 <213> ORGANISM: Aspergillus fumigatus
180 <400> SEQUENCE: 7
181 gccgcctctg cttcggttta ctgttccaac tcggccggca actacaagct gtcctccatc 60
183 gcagctccgg ttcaaggggc cggaaacccc ggctcggaat cgacctggca attgaccgtt 120
185 gacgacactt cgtccgggtca caaacagacg atagttaggt tcggtgctgc tgtcactgat 180
187 gccacgggtca cctcggttcaa cactttgtcc gcctccgtgc tgcaagactt gctcaataaa 240
189 ctgatgacac ctgccggggc gaactttgct ttgatgcgac atactattgg ggcttcggat 300
191 ctgtccggtg acccagccta cactgtacgat gacaatggtg ggaaagcgga tccgtcactg 360
193 tcgggattca acctggggga ccgcggaacg gctatggcca agatgttggc aacaatgaag 420
195 tctctgcagc ccaacctcaa gatcctcggc tctccctgga gtgcaccagg atggatgaag 480
197 ctgaacgggg tcttctgatg caatacgaac aacaacaact tgaacgatgg atacctaacc 540
199 agtgggggaa ccggtagtag ggggtatgcc agtcaattcg cgcagtactt tgtcaagtag 600
201 attcaggcct ataagaatct cgggtgtcac gtcgacgcga ttaccatcca gaacgagccg 660
203 ctgttcagct cagcgggcta tcccaccatg tatgtctacg attatgagtc ggcacagctg 720
205 atccagaact acatcggccc cgctcttgcc agcgcggggc tagatacggg aatctgggct 780
207 tatgaccaca acacagatgt cccgtcgtac ccccagactg tccttaacca ggccggtcag 840
209 tacgtcaagt cgggtggcctg gcaactgtac gctcccaacg tcgactggac cgtgtctcagc 900
211 cagttccaca acacaaaccc tggagtgaag caatatatga ccgagtgtct gactccagca 960
213 tctgggcgat ggcacagggc ggccggacttc accatgggtc ccctgcagaa ctgggcctcg 1020
215 ggagtggcag catggactct gggaaccaac gctcaggatg gtccgcactc gtccactggc 1080
217 ggctgcgcga catgtcaagg cttggtgacc atcaacaacg gaggatacac gctcaacacc 1140
219 gcatactaca tgatggcgca attcagcaag ttcatgccgc ctggtgcatg tgtgtcfaat 1200
221 ggcagtggca gctacacgta ctctggcgga ggcggtatcc agtccgtggc ttccttgaat 1260
223 cccgatggaa cccgcactgt ggttattgaa aacacttttg gcaatgatgt ctatgtgact 1320
225 gtcactatga agagcgggca gaagtggagt gggaacgccc ctagccaatc cgtgactacc 1380
227 tgggttcttc catctgcttg a
230 <210> SEQ ID NO: 8
231 <211> LENGTH: 466
232 <212> TYPE: PRT
233 <213> ORGANISM: Aspergillus fumigatus
235 <400> SEQUENCE: 8

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237 Ala Ala Ser Ala Ser Ala Tyr Cys Ser Asn Ser Ala Gly Asn Tyr Lys
238 1 5 10 15
241 Leu Ser Ser Ile Ala Ala Pro Val Gln Gly Ala Gly Asn Pro Gly Ser
242 20 25 30
245 Glu Ser Thr Trp Gln Leu Thr Val Asp Asp Thr Ser Ser Gly His Lys
246 35 40 45
249 Gln Thr Ile Val Gly Phe Gly Ala Ala Val Thr Asp Ala Thr Val Thr
250 50 55 60
253 Ser Phe Asn Thr Leu Ser Ala Ser Val Leu Gln Asp Leu Leu Asn Lys
254 65 70 75 80
257 Leu Met Thr Pro Ala Gly Ala Asn Phe Ala Leu Met Arg His Thr Ile
258 85 90 95
261 Gly Ala Ser Asp Leu Ser Gly Asp Pro Ala Tyr Thr Tyr Asp Asp Asn
262 100 105 110
265 Gly Gly Lys Ala Asp Pro Ser Leu Ser Gly Phe Asn Leu Gly Asp Arg
266 115 120 125
269 Gly Thr Ala Met Ala Lys Met Leu Ala Thr Met Lys Ser Leu Gln Pro
270 130 135 140
273 Asn Leu Lys Ile Leu Gly Ser Pro Trp Ser Ala Pro Gly Trp Met Lys
274 145 150 155 160
277 Leu Asn Gly Val Leu Asp Gly Asn Thr Asn Asn Asn Leu Asn Asp
278 165 170 175
281 Gly Tyr Leu Thr Ser Gly Gly Thr Gly Ser Thr Gly Tyr Ala Ser Gln
282 180 185 190
285 Phe Ala Gln Tyr Phe Val Lys Tyr Ile Gln Ala Tyr Lys Asn Leu Gly
286 195 200 205
289 Ala His Val Asp Ala Ile Thr Ile Gln Asn Glu Pro Leu Phe Ser Ser
290 210 215 220
293 Ala Gly Tyr Pro Thr Met Tyr Val Tyr Asp Tyr Glu Ser Ala Gln Leu
294 225 230 235 240
297 Ile Gln Asn Tyr Ile Gly Pro Ala Leu Ala Ser Ala Gly Leu Asp Thr
298 245 250 255
301 Glu Ile Trp Ala Tyr Asp His Asn Thr Asp Val Pro Ser Tyr Pro Gln
302 260 265 270
305 Thr Val Leu Asn Gln Ala Gly Gln Tyr Val Lys Ser Val Ala Trp His
306 275 280 285
309 Cys Tyr Ala Pro Asn Val Asp Trp Thr Val Leu Ser Gln Phe His Asn
310 290 295 300
313 Thr Asn Pro Gly Val Lys Gln Tyr Met Thr Glu Cys Trp Thr Pro Ala
314 305 310 315 320
317 Ser Gly Ala Trp His Gln Ala Ala Asp Phe Thr Met Gly Pro Leu Gln
318 325 330 335
321 Asn Trp Ala Ser Gly Val Ala Ala Trp Thr Leu Gly Thr Asn Ala Gln
322 340 345 350
325 Asp Gly Pro His Leu Ser Thr Gly Gly Cys Ala Thr Cys Gln Gly Leu
326 355 360 365
329 Val Thr Ile Asn Asn Gly Gly Tyr Thr Leu Asn Thr Ala Tyr Tyr Met
330 370 375 380
333 Met Ala Gln Phe Ser Lys Phe Met Pro Pro Gly Ala Ile Val Leu Asn

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334 385          390          395          400
337 Gly Ser Gly Ser Tyr Thr Tyr Ser Gly Gly Gly Ile Gln Ser Val
338          405          410          415
341 Ala Ser Leu Asn Pro Asp Gly Thr Arg Thr Val Val Ile Glu Asn Thr
342          420          425          430
345 Phe Gly Asn Asp Val Tyr Val Thr Val Thr Met Lys Ser Gly Gln Lys
346          435          440          445
349 Trp Ser Gly Asn Ala Pro Ser Gln Ser Val Thr Thr Trp Val Leu Pro
350          450          455          460
353 Ser Ala
354 465
357 <210> SEQ ID NO: 9
358 <211> LENGTH: 1647
359 <212> TYPE: DNA
360 <213> ORGANISM: Aspergillus fumigatus
362 <220> FEATURE:
363 <221> NAME/KEY: CDS
364 <222> LOCATION: (54)..(1517)
365 <223> OTHER INFORMATION:
368 <220> FEATURE:
369 <221> NAME/KEY: mat_peptide
370 <222> LOCATION: (120)..()
371 <223> OTHER INFORMATION:
374 <400> SEQUENCE: 9
375 ggcgacacca gaaagcaacc aagagcacga cacggactta tttctctttg aca atg      56
376                                     Met
379 cgt ata tct gtc ggt gct ctg ctt ggc ttg aca gcc ctg agt cat gcc      104
380 Arg Ile Ser Val Gly Ala Leu Leu Gly Leu Thr Ala Leu Ser His Ala
381   -20          -15          -10
383 aca aca gag aaa cga gcc gcc tct gct tcg gct tac tgt tcc aac tcg      152
384 Thr Thr Glu Lys Arg Ala Ala Ser Ala Ser Ala Tyr Cys Ser Asn Ser
385   -5          -1  1          5          10
387 gcc ggc aac tac aag ctg tcc tcc atc gca gct ccg gtt caa ggg gcc      200
388 Ala Gly Asn Tyr Lys Leu Ser Ser Ile Ala Ala Pro Val Gln Gly Ala
389          15          20          25
391 gga aac ccc ggc tcg gaa tcg acc tgg caa ttg acc gtt gac gac act      248
392 Gly Asn Pro Gly Ser Glu Ser Thr Trp Gln Leu Thr Val Asp Asp Thr
393          30          35          40
395 tcg tcc ggt cac aaa cag acg ata gtt ggg ttc ggt gct gct gtc act      296
396 Ser Ser Gly His Lys Gln Thr Ile Val Gly Phe Gly Ala Ala Val Thr
397          45          50          55
399 gat gcc acg gtc acc tcg ttc aac act ttg tcc gcc tcc gtg ctg caa      344
400 Asp Ala Thr Val Thr Ser Phe Asn Thr Leu Ser Ala Ser Val Leu Gln
401 60          65          70          75
403 gac ttg ctc aat aaa ctg atg aca cct gcc ggg gcg aac ttt gct ttg      392
404 Asp Leu Leu Asn Lys Leu Met Thr Pro Ala Gly Ala Asn Phe Ala Leu
405          80          85          90
407 atg cga cat act att ggg gct tcg gat ctg tcc ggt gac cca gcc tac      440
408 Met Arg His Thr Ile Gly Ala Ser Asp Leu Ser Gly Asp Pro Ala Tyr

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VERIFICATION SUMMARY

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Input Set : A:\Q63731 Sequence Listing.txt

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6